

**In the Claims**

Please replace all prior versions, and listings, of claims in the application with the following list of claims:

1. (Currently Amended) A method for identifying at least one human coding region/gene, including mutated or polymorphic variants thereof, which is associated with a bipolar disorder, comprising:

identifying the position of a coding region/gene in an 8.9 cM region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979 or a fragment thereof ~~in a that can be compared to an equivalent region of DNA from a person afflicted with a bipolar disorder~~, and

detecting differences between the coding region/gene ~~in the DNA of the 8.9 cM region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979 or a fragment thereof~~ one or more control individuals and ~~the coding region/gene equivalent region in the DNA of an individual afflicted with the a bipolar disorder~~, wherein a difference in the coding region/gene ~~in the DNA of the one or more control individuals and the coding region/gene in the DNA of the individual afflicted with the bipolar disorder equivalent region~~ identifies the coding region/gene or mutated or polymorphic variant thereof as associated with the bipolar disorder.

2. (Currently Amended) A method for identifying at least one human coding region/gene, including mutated or polymorphic variants thereof, which is associated with a bipolar disorder, comprising:

identifying the position of a control coding region/gene in a YAC clone comprising a portion of human chromosome 18q disposed between polymorphic markers D18S60 and D18S61 ~~that can be compared to an equivalent region of DNA from a person afflicted with the a bipolar disorder~~, and

detecting differences between the control coding region/gene of the YAC clone comprising a portion of human chromosome 18q disposed between polymorphic markers D18S60 and D18S61 and the coding region/gene equivalent region of DNA of an individual

afflicted with the a bipolar disorder, wherein a difference in the control coding region/gene and the coding region/gene of DNA of the individual afflicted with a bipolar disorder equivalent region of DNA identifies that the coding region/gene or mutated or polymorphic variant thereof is associated with the bipolar disorder.

3. (Previously Presented) The method of claim 2 wherein said portion comprises the region of chromosome 18q between polymorphic markers D18S68 and D18S979 or a fragment of said region.

4. (Previously Presented) The method of claim 2 wherein said YAC clone is 961\_h\_9, 942\_c\_3, 766\_f\_12, 731\_c\_7, 907\_e\_1, 752\_g\_8 or 717\_d\_3.

5. (Previously Presented) The method of claim 4 wherein said YAC clone is 961\_h\_9, 766\_f\_12 or 907\_e\_1.

6-47. (Cancelled)